SEQUENCE LISTING

<110> Medical Research Company
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<120> Recombinant Nematode Nicotinic Receptor and Uses

<130> 18396/2112

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<151> 2000-06-09

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<151> 1999-06-09

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<170> PatentIn Ver. 3.3

<210> 1
<211> 502
<212> PRT
<213> Caenorhabditis elegans

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Met Gly Pro Asn Asp His Gly Phe Ala Tyr Ile Leu Ile Phe Leu Leu
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Leu Ser Pro Pro Thr His Ala Asn Arg Asp Ala Asn Arg Leu Phe Glu
            20                  25                  30

Asp Leu Ile Ala Asp Tyr Asn Lys Leu Val Arg Pro Val Ser Glu Asn
        35                  40                  45

Gly Glu Thr Leu Val Val Thr Phe Lys Leu Lys Leu Ser Gln Leu Leu
    50                  55                  60

Asp Val His Glu Lys Asn Gln Ile Met Thr Thr Asn Val Trp Leu Gln
65                  70                  75                  80

His Ser Trp Met Asp Tyr Lys Leu Arg Trp Asp Pro Val Glu Tyr Gly
                85                  90                  95

Gly Val Glu Val Leu Tyr Val Pro Ser Asp Thr Ile Trp Leu Pro Asp
            100                 105                 110

Val Val Leu Tyr Asn Asn Ala Asp Gly Asn Tyr Gln Val Thr Ile Met
        115                 120                 125

Thr Lys Ala Lys Leu Thr Tyr Asn Gly Thr Val Glu Trp Ala Pro Pro
    130                 135                 140

Ala Ile Tyr Lys Ser Met Cys Gln Ile Asp Val Glu Phe Phe Pro Phe
145                 150                 155                 160

Asp Arg Gln Gln Cys Glu Met Lys Phe Gly Ser Trp Thr Tyr Gly Gly
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                 165                 170                 175

Leu Glu Val Asp Leu Gln His Arg Asp Lys His Leu Glu Lys Glu Ile
            180                 185                 190

Glu Glu Asp Val Glu Gly Val Asp Gly Pro Thr Lys Glu Ile Val Trp
        195                 200                 205

Val Val Asp Arg Gly Ile Asp Leu Ser Asp Tyr Tyr Pro Ser Val Glu
    210                 215                 220

Trp Asp Ile Leu Asn Val Pro Gly Lys Arg His Ser Lys Arg Tyr Pro
225                 230                 235                 240

Cys Cys Glu Ser Pro Phe Ile Asp Ile Thr Tyr Glu Ile His Leu Arg
                245                 250                 255

Arg Lys Thr Leu Phe Tyr Thr Val Asn Leu Ile Phe Pro Ser Val Gly
            260                 265                 270

Ile Ser Phe Leu Thr Ala Leu Val Phe Tyr Leu Pro Ser Asp Gly Gly
        275                 280                 285

Glu Lys Ile Ser Leu Cys Ile Ser Ile Leu Ile Ser Leu Thr Val Phe
    290                 295                 300

Phe Leu Leu Leu Val Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro
305                 310                 315                 320

Leu Ile Gly Lys Tyr Leu Leu Phe Thr Met Val Leu Val Thr Leu Ser
                325                 330                 335

Val Val Val Thr Val Val Thr Leu Asn Val His Tyr Arg Ser Pro Thr
            340                 345                 350

Thr His Thr Met Pro Lys Trp Met Lys Arg Leu Phe Val Asp Phe Leu
        355                 360                 365

Pro Lys Tyr Leu Leu Met Thr Arg Pro Gln Pro Pro Gly His His Ser
    370                 375                 380

Lys Pro Asn Arg Lys Phe Asp Ser Arg Ala Ser Thr Phe Ser Ile Gly
385                 390                 395                 400

Val Asn His Val Leu Gly Gln Asn Ser Glu Leu Leu Ser Pro Gly Leu
                405                 410                 415

Asn Ser Asn Arg Glu Glu Ser Ser Phe Thr Leu Pro Arg Asp Asn Ser
            420                 425                 430

Pro Val Arg Ser Ala Val Glu Ser Val Ala Tyr Ile Ala Asp His Leu
        435                 440                 445

Lys Asn Glu Glu Asp Asp Lys Gln Val Ile Glu Asp Trp Lys Tyr Ile
    450                 455                 460

Ser Val Val Met Asp Arg Ile Phe Leu Ile Thr Phe Thr Phe Ala Cys
465                 470                 475                 480

Ala Phe Gly Thr Val Val Ile Ile Ala Arg Ala Pro Ser Ile Tyr Asp
                485                 490                 495

Asn Thr Pro Ala Leu Ala
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<210> 2
<211> 513
<212> PRT
<213> Caenorhabditis elegans

<220>
<221> MISC_FEATURE
<222> (86)..(109); (206)..(225); (322)..(345); (430)..(452)
<223> Xaa at these positions can be any amino acid.

<400> 2

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Met Arg Ser Phe Trp Leu Phe Leu Leu Leu Leu Phe Cys Ile Ser
  1               5                  10                  15

Phe Ile Lys Leu Thr Glu Gly Asn Glu Asp Ala Lys Arg Leu Tyr Asp
            20                  25                  30

Asp Leu Met Val Asn Tyr Asn Arg His Arg Arg Pro Ser Thr Ser Pro
        35                  40                  45

Asn Lys Pro Leu Thr Ile Lys Leu Lys Leu Lys Leu Arg Leu Ser Gln
    50                  55                  60

Ile Ile Asp Val His Glu Ile Asp Gln Ile Met Thr Cys Ser Val Trp
65                  70                  75                  80

Leu Lys Gln Thr Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                85                  90                  95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Trp Val
            100                 105                 110

Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Ser Asn Tyr Asn Ile Thr
        115                 120                 125

Ile Ser Thr Lys Ala Thr Leu His Tyr Thr Gly Glu Val Thr Trp Glu
    130                 135                 140

Pro Pro Ala Ile Phe Lys Ser Met Cys Gln Ile Asp Val Arg Trp Phe
145                 150                 155                 160

Pro Phe Asp Glu Gln Gln Cys His Leu Lys Phe Gly Ser Trp Thr Phe
                165                 170                 175

Ser Glu Asn Leu Leu Ser Val Glu Leu Asn Glu Pro Ser Leu Arg Tyr
            180                 185                 190

Glu Glu Glu Ile Asp Glu Lys Gly Ile Ile Asp Asn Val Xaa Xaa Xaa
        195                 200                 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    210                 215                 220

Xaa Met Ser Arg Val Ala Lys Arg Arg Ala Lys Asn Tyr Pro Ser Cys
225                 230                 235                 240

Cys Pro Gln Ser Ala Tyr Ile Asp Val Thr Tyr Tyr Leu Gln Leu Arg
                245                 250                 255

Arg Lys Pro Leu Phe Tyr Thr Val Asn Leu Val Phe Pro Cys Val Gly
```

```
            260                 265                 270

Ile Ser Phe Leu Thr Ile Leu Val Phe Tyr Leu Pro Ser Asp Ser Gly
        275                 280                 285

Glu Lys Val Thr Leu Cys Ile Ser Ile Leu Val Ala Leu Thr Ile Phe
    290                 295                 300

Phe Leu Leu Leu Thr Glu Ile Ile Pro Ala Thr Ser Ile Thr Leu Pro
305                 310                 315                 320

Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                325                 330                 335

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu His Phe Arg Thr Pro Thr
            340                 345                 350

Thr His Leu Met Pro Asn Trp Val Lys Lys Val Phe Leu Lys Trp Leu
        355                 360                 365

Pro Lys Leu Leu Phe Met Arg Arg Pro Ile Asp Asp Tyr Glu Glu Lys
    370                 375                 380

Phe Asp Asp Lys Lys Lys Pro Lys Asp Gly Lys Ile Ala Leu Ser Val
385                 390                 395                 400

His Ala His Arg Val Ser Asn Val Gly Asn Asn Ile Arg Asn Ala Thr
                405                 410                 415

Ile Asp Asp Thr Ile Gln Lys Met Tyr Tyr Ser Pro Pro Xaa Xaa Xaa
            420                 425                 430

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        435                 440                 445

Xaa Xaa Xaa Xaa Ile Asp Glu Asp Trp Lys Tyr Val Ala Met Val Leu
    450                 455                 460

Asp Arg Leu Phe Leu Leu Ile Phe Ser Ile Ala Cys Phe Val Gly Thr
465                 470                 475                 480

Val Ile Ile Leu Leu Arg Ala Pro Thr Leu Tyr Asp Thr Arg Gln Pro
                485                 490                 495

Ile Asp Leu Gln Tyr Arg Pro Ala Asn Leu Ser Ala Asn Pro Ile Ser
            500                 505                 510

Phe


<210> 3
<211> 507
<212> PRT
<213> Caenorhabditis elegans

<220>
<221>  MISC_FEATURE
<222>  (96)..(119); (196).. (214); (301)..(324); (417)..(439)
<223>  Xaa at these positions can be any amino acid.

<400> 3
Met Met Leu Gly Gly Gly Gly Gly Cys Gly Ala Gly Gly Thr Trp Leu
  1               5                  10                  15
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Gly Phe Leu Val Phe Leu Ala Val Ser Leu Arg Asn His Ser Thr Cys
20 25 30

Glu Asp Ile Asp Ala Glu Asp Arg Leu Met Val Asp Leu Phe Arg Gly
35 40 45

Tyr Asn Ser Leu Val Gln Pro Val Arg Asn Arg Ser Glu Leu Pro Met
50 55 60

Ile Val Lys Ile Gly Met Gln Leu Val Leu Leu Ile Asn Val Asp Glu
65 70 75 80

Lys Glu Gln Val Met His Thr Asn Val Trp Leu Thr Met Lys Trp Xaa
85 90 95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Trp Leu Pro Asp Ile Val Leu Phe
115 120 125

Asn Asn Ala Asp Gly Asn Tyr Glu Val Ser Phe Met Cys Asn Val Leu
130 135 140

Ile Leu Ser Thr Gly Thr Val Leu Trp Val Pro Pro Ala Ile Tyr Lys
145 150 155 160

Ser Ser Cys Ile Ile Asp Val Glu Phe Phe Pro Phe Asp Asp Gln Leu
165 170 175

Cys Ser Leu Thr Phe Gly Ser Trp Thr Tyr Asn Arg Asp Glu Ile Lys
180 185 190

Leu Asp Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Met Asp Gly Pro Ala Val Leu Thr Ser Asp
210 215 220

Arg Ser Arg Ile Glu Phe Gln Ile Arg Ile Arg Arg Lys Thr Leu Phe
225 230 235 240

Tyr Thr Val Val Leu Ile Leu Pro Thr Val Leu Met Ala Phe Leu Asn
245 250 255

Val Thr Val Phe Tyr Leu Pro Thr Ala Ser Gly Glu Lys Met Gly Leu
260 265 270

Thr Met Asn Val Leu Leu Ser Ile Val Val Phe Leu Leu Leu Val Ser
275 280 285

Lys Ile Leu Pro Pro Thr Ser Ser Ser Ile Pro Leu Xaa Xaa Xaa Xaa
290 295 300

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
305 310 315 320

Xaa Xaa Xaa Xaa Ile Tyr Phe Arg Ser Pro Ile Thr His Arg Leu Pro
325 330 335

Pro Trp Val Arg Lys Val Phe Leu Asp Ile Leu Pro Leu Leu Met Cys
340 345 350

```
Met Gln Arg Pro His Arg Lys Asn Val Ile Gln Arg Ser His Arg Arg
        355                 360                 365

Leu Leu Glu Thr Gly Pro Ser Val Glu Glu Asn Pro Met Arg Ser Gly
    370                 375                 380

Glu His His Pro Leu Cys Arg His Thr His Asn Gln Asp Ser Cys Arg
385                 390                 395                 400

Arg Val Arg Ile Gln Ser Asp Glu Leu Asp Asp Glu Leu Ser Pro Glu
                405                 410                 415

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            420                 425                 430

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Arg Asp Asp Trp Lys Phe Ile Ala
        435                 440                 445

Ser Val Val Asp Arg Phe Leu Leu Tyr Gly Phe Phe Gly Ala Thr Val
    450                 455                 460

Gly Gly Thr Ile Gly Ile Ile Phe Thr Ala Pro Ser Val Phe Glu Thr
465                 470                 475                 480

Phe Asp Glu Asn Ala Thr Leu Val Lys Leu Lys Gln Leu Tyr Asp Met
                485                 490                 495

Gly Leu Ala Asn Asp Thr Val Leu Gly Ile Phe
            500                 505


<210> 4
<211> 493
<212> PRT
<213> Caenorhabditis elegans

<220>
<221>  MISC_FEATURE
<222>  (88).. (111); (188)..(206); (292)..(316); (409)..(431)
<223>  Xaa at these positions can be any amino acid.

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Met Arg Thr Asn Arg Leu Ser Trp Ile Leu Val Leu Ser Val Val Ile
  1               5                  10                  15

Phe Leu Val Ile Ile Asn Thr Ile Asn Ala Ser Asp Asp Glu Glu Arg
             20                  25                  30

Leu Met Val Asp Val Phe Arg Gly Tyr Asn Ser Leu Ile Gln Pro Val
         35                  40                  45

Arg Asn Ser Ser Glu Leu Pro Leu Ile Val Lys Met Ala Leu Gln Leu
     50                  55                  60

Val Leu Leu Ile Asn Val Asp Glu Lys Asp Gln Val Met His Thr Asn
 65                  70                  75                  80

Val Trp Leu Thr Leu Gln Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                 85                  90                  95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val
            100                 105                 110
```

Trp Leu Pro Asp Ile Val Leu Phe Asn Asn Ala Asp Gly Asn Tyr Glu
115 120 125

Val Ser Phe Met Cys Asn Val Val Ile Asn His Lys Gly Asp Met Leu
130 135 140

Trp Val Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ile Ile Asp Val Glu
145 150 155 160

Phe Phe Pro Phe Asp Glu Gln Val Cys Thr Leu Val Phe Gly Ser Trp
165 170 175

Thr Tyr Asn Glu Asn Glu Ile Lys Leu Glu Phe Xaa Xaa Xaa Xaa Xaa
180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Asp
195 200 205

Val Pro Ala Ser Leu Val Asn Lys Arg Ser Arg Ile Glu Phe Gln Val
210 215 220

Arg Ile Arg Arg Lys Thr Leu Phe Tyr Thr Val Val Leu Ile Ile Pro
225 230 235 240

Thr Val Leu Met Ala Phe Leu Ser Met Ala Val Phe Phe Leu Pro Thr
245 250 255

Asp Ser Gly Glu Lys Ile Thr Leu Thr Ile Ser Val Leu Leu Ser Ile
260 265 270

Val Val Phe Leu Leu Leu Val Ser Lys Ile Leu Pro Pro Thr Ser Ser
275 280 285

Thr Ile Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
290 295 300

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Tyr Phe Arg
305 310 315 320

Gly Pro Arg Thr His Arg Met Pro Gln Trp Val Arg Val Val Phe Leu
325 330 335

Gln Phe Leu Pro Lys Leu Val Cys Met Lys Arg Pro Lys Ser Ala Ser
340 345 350

Glu Arg Ser Ala Val Arg Ser Gly Met Ala Gln Leu Pro Gly Val Gly
355 360 365

Gln Phe Thr Leu Ser Pro Ser Ala His His Pro Leu Cys Pro Ser Ala
370 375 380

Asp Asp Arg Thr Thr Thr Ile Arg Asn Thr Ala Ser Asn Glu Thr Ser
385 390 395 400

Ala Tyr Tyr Pro Leu Ser Thr Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
405 410 415

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe
420 425 430

Arg Asp Asp Trp Lys Tyr Val Ala Met Ile Ile Asp Arg Leu Leu Leu
435 440 445

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Tyr Val Phe Phe Gly Ile Thr Val Gly Gly Thr Cys Gly Ile Leu Phe
    450                 455                 460

Ser Ala Pro His Val Phe Gln Arg Ile Asp Gln Gln Glu Met Leu Asp
465                 470                 475                 480

Arg Leu Lys Glu Lys Tyr Asp Thr Ala Ser Asn Ile Pro
                485                 490
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